

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 7, 2002, 10:03:04 : Search time 27.2727 Seconds  
(without alignments)  
4034.242 Million cell updates/sec

Title: US-09-125-005-6  
Perfect score: 3384

Sequence: 1 MAQSTATSPDGGTTFEHLWS.....PDKARKQPIKEEFTAEIHH 636

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL19.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Match | Length | DB | ID     | Description         |
|------------|--------|-------|--------|----|--------|---------------------|
| 1          | 3014.5 | 89.1  | 631    | 11 | Q9JJP2 | Q9JJP2 mus musculus |
| 2          | 2830.5 | 83.6  | 590    | 11 | Q9JJP1 | Q9JJP1 mus musculus |
| 3          | 2507.5 | 74.1  | 514    | 11 | Q9CU77 | Q9CU77 mus musculus |
| 4          | 2414.5 | 71.4  | 641    | 13 | Q9W664 | Q9W664 barbus barb  |
| 5          | 2379   | 70.3  | 497    | 11 | Q9WUJ0 | Q9WUJ0 mus musculus |
| 6          | 1790   | 52.9  | 641    | 4  | Q9UP28 | Q9UP28 homo sapien  |
| 7          | 1790   | 52.9  | 680    | 4  | Q9H3D4 | Q9H3D4 homo sapien  |
| 8          | 1789   | 52.9  | 663    | 11 | Q9JJE3 | Q9JJE3 rattus norv  |
| 9          | 1789   | 52.9  | 680    | 11 | Q88898 | Q88898 mus musculus |
| 10         | 1789   | 52.9  | 680    | 11 | Q9JJP6 | Q9JJP6 rattus norv  |
| 11         | 1786   | 52.8  | 641    | 4  | O75195 | O75195 homo sapien  |
| 12         | 1782   | 52.7  | 680    | 4  | Q9UE10 | Q9UE10 homo sapien  |
| 13         | 1743   | 51.5  | 586    | 11 | O89097 | O89097 mus musculus |
| 14         | 1741   | 51.4  | 586    | 4  | Q9UBV9 | Q9UBV9 homo sapien  |
| 15         | 1740   | 51.4  | 586    | 11 | Q9JJE2 | Q9JJE2 rattus norv  |
| 16         | 1737   | 51.3  | 586    | 4  | Q9P1B4 | Q9P1B4 homo sapien  |

|    |        |      |     |    |        |                     |
|----|--------|------|-----|----|--------|---------------------|
| 17 | 1727   | 51.0 | 586 | 4  | O75080 | O75080 homo sapien  |
| 18 | 1698.5 | 50.2 | 582 | 13 | Q9DEC7 | Q9DEC7 gallus gall  |
| 19 | 1470.5 | 43.5 | 501 | 4  | Q9H3P8 | Q9H3P8 homo sapien  |
| 20 | 1464.5 | 43.3 | 516 | 4  | Q9P1B7 | Q9P1B7 homo sapien  |
| 21 | 1464.5 | 43.3 | 516 | 4  | Q9UP27 | Q9UP27 homo sapien  |
| 22 | 1464.5 | 43.3 | 555 | 4  | Q9H3D3 | Q9H3D3 homo sapien  |
| 23 | 1459.5 | 43.1 | 538 | 11 | Q9JJD7 | Q9JJD7 rattus norv  |
| 24 | 1459.5 | 43.1 | 555 | 11 | Q9QWZ0 | Q9QWZ0 mus musculus |
| 25 | 1459.5 | 43.1 | 555 | 11 | Q9JJD8 | Q9JJD8 rattus norv  |
| 26 | 1415.5 | 41.8 | 461 | 4  | Q9P1B5 | Q9P1B5 homo sapien  |
| 27 | 1415.5 | 41.8 | 461 | 4  | Q9UP26 | Q9UP26 homo sapien  |
| 28 | 1413.5 | 41.8 | 461 | 11 | Q9QWY9 | Q9QWY9 mus musculus |
| 29 | 1410.5 | 41.7 | 461 | 11 | Q9JJD6 | Q9JJD6 rattus norv  |
| 30 | 1385   | 40.9 | 471 | 4  | Q9NPH7 | Q9NPH7 homo sapien  |
| 31 | 1336   | 39.5 | 416 | 4  | Q9P1B6 | Q9P1B6 homo sapien  |
| 32 | 1335.5 | 39.5 | 286 | 11 | Q9D6A3 | Q9D6A3 mus musculus |
| 33 | 1302.5 | 38.5 | 470 | 11 | Q9JJE1 | Q9JJE1 rattus norv  |
| 34 | 1302.5 | 38.5 | 487 | 11 | Q9JJE0 | Q9JJE0 rattus norv  |
| 35 | 1297.5 | 38.3 | 448 | 4  | O76078 | O76078 homo sapien  |
| 36 | 1297.5 | 38.3 | 487 | 4  | Q9H3D2 | Q9H3D2 homo sapien  |
| 37 | 1284.5 | 38.0 | 483 | 11 | O88897 | O88897 mus musculus |
| 38 | 1253.5 | 37.0 | 393 | 11 | Q9JJD9 | Q9JJD9 rattus norv  |
| 39 | 1248.5 | 36.9 | 393 | 4  | O75922 | O75922 homo sapien  |
| 40 | 1240.5 | 36.7 | 356 | 4  | Q9OP74 | Q9OP74 homo sapien  |
| 41 | 1238.5 | 36.6 | 389 | 11 | O88899 | O88899 mus musculus |
| 42 | 1237.5 | 36.5 | 365 | 13 | Q98SW0 | Q98SW0 xenopus lae  |
| 43 | 994    | 29.4 | 232 | 4  | Q96KRO | Q96KRO homo sapien  |
| 44 | 905.5  | 26.8 | 621 | 5  | Q9NGC7 | Q9NGC7 mya arenari  |
| 45 | 859.5  | 25.4 | 564 | 5  | Q27937 | Q27937 loligo forb  |

## ALIGNMENTS

RESULT 1

Q9JJP2 ID Q9JJP2 PRELIMINARY; PRT; 631 AA.  
AC Q9JJP2  
DT 01-OCT-2000 (TREMREL. 15, Created)  
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)  
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)  
DE P73 ALPHA PROTEIN.  
GN TRP73 OR P73  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20179195; PubMed=10716451;  
RA Yang A., Walker N., Bronson R., Kaghad M., Oosterweel M., Bonnin J.,  
Vagner C., Bonnet H., Dikkes P., Sharpe A., McKee F., Caput D.;  
RT "p73-deficient mice have neurological, phenomonal and inflammatory  
defects but lack spontaneous tumors.";  
RL Nature 404:99-103(2000).  
DR EMBL; Y19234; CAB81953.1;  
DR HSSP; O15350; 1COK.  
DR MGD; MGI:1336991; Trp73  
DR InterPro; IPR002117; P53.  
DR InterPro; IPR001660; SAM.  
DR Pfam; PF00870; P53; 1.  
DR Pfam; PF00536; SAM; 1.  
DR PRINTS; PR00386; P53SUPPRESSR.  
DR PRODOM; PD002681; P53; 1.  
DR SMART; SM00454; SAM; 1.  
DR PROSITE; PS00346; P53; UNKNOWN\_1.  
SQ SEQUENCE 631 AA; 69095 MW; E364D566A90CBF1D CRC64;

Query Match 89.1%; Score 3014.5; DB 11; Length 631;  
Best Local Similarity 88.8%; Pred. No. 3.6e-241;  
Matches 569; Conservative 25; Mismatches 32; Indels 15; Gaps 6;

QY 1 MAQSTATSPDGGTTFEHLWSLEPDTSTYFDLPQSSRGNNVGGTSSMDVFLHLEGMTTS 60

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Db 1 MAQ-----TSSSSSTFEHLWSLESDSYFDLPQSQSTSEASSESNMDVFLQG---- 53
QY 61 VMAQFNLLSSTMDQSSRAASAPYTPTEHAASVPTHTSPYAQPSSTEDTMSAPVIPSNTD 120
Db 54 -MAQFNLLSSAMDQSSRAAPSPYTPTEHAASAPHTSPYAQPSSTEDTMSAPVIPSNTD 112
QY 121 YGPHHEFVTFQOSTAKSATWTYSPLLKLYCOIAKTCPIQIKVSTPPPGTAIRAMPV 180
Db 113 YGPHHEFVTFQOSTAKSATWTYSPLLKLYCOIAKTCPIQIKVSTPPPGTAIRAMPV 172
QY 181 YKKAHVTDVVKRCPNHGLRDNFEGOSAPASHLIRVEGNLLSQYVDDPVTGRQSVVVPY 240
Db 173 YKKAHVTDVVKRCPNHGLRDNFEGOSAPASHLIRVEGNLLSQYVDDPVTGRQSVVVPY 232
QY 241 EPPQVGTFTILYNFACNSCVGMNRRPILIIITLMDRGQVLGRSFEGRICACPGR 300
Db 233 EPPQVGTFTILYNFACNSCVGMNRRPILIIITLMDRGQVLGRSFEGRICACPGR 292
QY 301 DRKADEHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRRHGDDETYTLOVR 360
Db 293 DRKADEHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRRHGDDETYTLOVR 352
QY 361 GRENEFILLKLESLELMELVPOPLVDYSR--QQQLLQRPRLSHLPSPYGPVLSMKNVH 418
Db 353 GRENEFILLKLESLELMELVPOPLVDYSR--QQQLLQRPRLSHLPSPYGPVLSMKNVH 412
QY 419 GGNKLPVSNOLVQPPPHSSAAATPNLGPVPGMLNHHGAVPANGEMSSSHSAQSVYSG 478
Db 413 GGNKLPVSNOLVQPPPHSSAAATPNLGPVPGMLNHHGAVPANGEMSSSHSAQSVYSG 472
QY 479 SHCTPPPYHADPSLVSLTGLGCPNCEIYFTSQGLQSIYHLQNLTIEDLGALKIPEQYR 538
Db 473 SHCTPPPYHADPSLVSLTGLGCPNCEIYFTSQGLQSIYHLQNLTIEDLGALKIPEQYR 532
QY 539 MTIWGLQDLKQGHDXSTAQQLLR--SSNAATISIGSGELQORVMEAVHFRVHTITIP 597
Db 533 MTIWGLQDLKQGHDXSTAQQLLR--SSNAATISIGSGELQORVMEAVHFRVHTITIP 590
QY 598 NRGPGG--GPDEWADFGDLPDCKARKQPIKEEFTAEI 636
Db 591 NRGPGG--GPDEWADFGDLPDCKARKQPIKEEFTAEI 631

RESULT 2
Q9CU77 ID Q9CU77 PRELIMINARY; PRT; 590 AA.
AC Q9CU77;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE P73 DELTA-N PROTEIN.
GN TRP73 OR P73.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20179195; PubMed=10716451;
RA Yang A., Walker N., Bronson R., Kaghad M., Osterweil M., Bonnin J.,
RA Wagner C., Bonnet H., Dikkes P., Sharpe A., McKeon F., Caput D.;
RT "p73-deficient mice have neurological, pheomonal and inflammatory
RT defects but lack spontaneous tumors.;"
RL Nature 404:99-103(2000).
DR EMBL: Y19235; CAB81954.1;
DR HSSP: O15350; ICKO;
DR MGD: MGI:1336991; Trp73.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam: PF00870; P53; 1.
DR Pfam: PF00536; SAM; 1.
DR PRINTS: PR00386; P53SUPPRESSOR.

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ProDom; PD002681; P53; 1.
DR SMART; SMO0454; SAM; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 590 AA: 64725 MW: 8580C7BFA21B5797 CRC64;

Query Match 83.68; Score 2830.5; DB 11; Length 590;
Best Local Similarity 91.7%; Pred. No. 5.8e-226;
Matches 531; Conservative 19; Mismatches 22; Indels 7; Gaps 4;

QY 63 AOFNLLSSTMDQSSRAASAPYTPTEHAASVPTHTSPYAQPSSTEDTMSAPVIPSNTDYP 122
Db 14 AOFNLLSSAMDQSSRAAPSPYTPTEHAASAPHTSPYAQPSSTEDTMSAPVIPSNTDYP 73
QY 123 GRPHHEFVTFQOSTAKSATWTYSPLLKLYCOIAKTCPIQIKVSTPPPGTAIRAMPV 182
Db 74 GRPHHEFVTFQOSTAKSATWTYSPLLKLYCOIAKTCPIQIKVSTPPPGTAIRAMPV 133
QY 183 KAHEVTDVVKRCPNHGLRDNFEGOSAPASHLIRVEGNLLSQYVDDPVTGRQSVVVPY 242
Db 134 KAHEVTDVVKRCPNHGLRDNFEGOSAPASHLIRVEGNLLSQYVDDPVTGRQSVVVPY 193
QY 243 PQVGTFTILYNFACNSCVGMNRRPILIIITLMDRGQVLGRSFEGRICACPGRDR 302
Db 194 PQVGTFTILYNFACNSCVGMNRRPILIIITLMDRGQVLGRSFEGRICACPGRDR 253
QY 303 KADEHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRRHGDDETYTLOVR 362
Db 254 KADEHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRRHGDDETYTLOVR 313
QY 363 ENFEILLKLESLELMELVPOPLVDYSR--QQQLLQRPRLSHLPSPYGPVLSMKNVHGG 420
Db 314 ENFEILLKLESLELMELVPOPLVDYSR--QQQLLQRPRLSHLPSPYGPVLSMKNVHGG 373
QY 421 MNKLPVSNOLVQPPPHSSAAATPNLGPVPGMLNHHGAVPANGEMSSSHSAQSVYSGSH 480
Db 374 MNKLPVSNOLVQPPPHSSAAATPNLGPVPGMLNHHGAVPANGEMSSSHSAQSVYSGSH 433
QY 481 CTPPPPYHADPSLVSLTGLGCPNCEIYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMT 540
Db 434 CTPPPPYHADPSLVSLTGLGCPNCEIYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMT 493
QY 541 IWRGLQDLKQGHDXSTAQQLLR--SSNAATISIGSGELQORVMEAVHFRVHTITIPNR 599
Db 494 IWRGLQDLKQGHDXSTAQQLLR--SSNAATISIGSGELQORVMEAVHFRVHTITIPNR 551
QY 600 GPGG--GPDEWADFGDLPDCKARKQPIKEEFTAEI 636
Db 552 GPGG--GPDEWADFGDLPDCKARKQPIKEEFTAEI 631

RESULT 3
Q9CU77 ID Q9CU77 PRELIMINARY; PRT; 514 AA.
AC Q9CU77;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE TRANSFORMATION RELATED PROTEIN 73 (FRAGMENT).
GN TRP73...
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

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RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schramm L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 DR EMBL; AK017412; BAB30732.1;  
 DR HSSP; O15350; ICOK.  
 DR MGD; MGI:1336991; Trp73.  
 DR InterPro; IPR002117; P53.  
 DR InterPro; IPR001660; SAM.  
 DR Pfam; PF00870; P53; 1.  
 DR Pfam; PF00536; SAM; 1.  
 DR PRINTS; PR00386; P53SOPPRESSR.  
 DR PRODOM; PD002681; P53; 1.  
 DR SMART; SM00454; SAM; 1.  
 DR PROSITE; PS00348; P53; UNKNOWN\_1.  
 DR NON\_TER; 1;  
 FT  
 SQ SEQUENCE 514 AA; 56677 MW; 539AE64527CBF552 CRC64;

Query Match 74.1%; Score 2507.5; DB 11; Length 514;  
 Best Local Similarity 91.5%; Pred. No. 2.8e-199;  
 Matches 471; Conservative 19; Mismatches 18; Indels 7; Gaps 4;

QY 127 FEVTFQSSSTAKSATWYSPLLKLYCQIAKTCPIQIKVSTPPPTAIRAMPVYKKAH 186  
 DB 2 FEVTFQSSSTAKSATWYSPLLKLYCQIAKTCPIQIKVSTPPPTAIRAMPVYKKAH 61  
 QY 187 VTDVVKPCNHELGRDNFEGOSAPASHLRVEGNLSQYVDDPVTGROSVVVYPPQVG 246  
 DB 62 VTDVVKPCNHELGRDNFEGOSAPASHLRVEGNLSQYVDDPVTGROSVVVYPPQVG 121  
 QY 247 TEFTILYNFNCSSCVGGMNRRLIITLEMRDGOVLGRSFGRICACGRDRKADE 306  
 DB 122 TEFTILYNFNCSSCVGGMNRRLIITLEMRDGOVLGRSFGRICACGRDRKADE 181  
 QY 307 DHYREQOALNESSAKGAAKRAFKQSPAPALGAGVKKRRHGDEDTYILQVRGRENFE 366  
 DB 182 DHYREQOALNESSAKGAAKRAFKQSPAPALGAGVKKRRHGDEDTYILQVRGRENFE 241  
 QY 367 ILMKLESLELMELVLPQPLVDSYR--QQOQLQRPSPVPGVPLSPMKVHGGMKL 424  
 DB 242 ILMKLESLELMELVLPQPLVDSYR--QQOQLQRPSPVPGVPLSPMKVHGGMKL 301  
 QY 425 PVSQVNLVQPPPHSSAATPNLGPVGMNNHGHAYPANGEMSSSSAQSMVSGSHCTPP 484  
 DB 302 PVSQVNLVQPPPHSSAATPNLGPVGMNNHGHAYPANGEMSSSSAQSMVSGSHCTPP 361  
 QY 485 PPYHADPSLVFLGLGCPNCIEFTSQGLQSIYHLQNTIEDLGALKIPDYRTIWRG 544  
 DB 362 PPYHADPSLVFLGLGCPNCIEFTSQGLQSIYHLQNTIEDLGALKIPDYRTIWRG 421  
 QY 545 LODLKQGHDSYTAQQLLR--SSNAATISIGSGELQORVMEVHFVRRTIIPNRGGP 603  
 DB 422 LODLKQGHDSYTAQQLLR--SSNAATISIGSGELQORVMEVHFVRRTIIPNRGGP 479  
 QY 604 G--GPDEWADFGDLPCKARKQPIKEEFTAEIH 636  
 DB 480 AVTGPDEWADFGDLPCKARKQPIKEEFTAEIH 514

## RESULT 4

Q9W664  
 ID Q9W664  
 AC Q9W664;

PRELIMINARY; PRT; 641 AA.

DT 01-NOV-1999 (TREMREL.12, Created)  
 DT 01-NOV-1999 (TREMREL.12, Last sequence update)  
 DT 01-DEC-2001 (TREMREL.19, Last annotation update)  
 DE P73.  
 OS Barbus barbus (Barbel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Barbus.  
 OX NCBI\_TaxID=40830;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20362516; PubMed=10825664;  
 RA Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;  
 RT "Molecular Characterization of the first non-mammalian p73 cDNA.";  
 RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 126:49-57(2000).  
 DR EMBL; AF043641; AAD27752.1;  
 DR HSSP; O15350; ICOK.  
 DR InterPro; IPR002117; P53.  
 DR InterPro; IPR001660; SAM.  
 DR Pfam; PF00870; P53; 1.  
 DR Pfam; PF00536; SAM; 1.  
 DR PRINTS; PR00386; P53SOPPRESSR.  
 DR PRODOM; PD002681; P53; 1.  
 DR SMART; SM00454; SAM; 1.  
 SQ SEQUENCE 641 AA; 71090 MW; 4A215B21AEB16E4D CRC64;

Query Match 71.4%; Score 2414.5; DB 13; Length 641;  
 Best Local Similarity 70.7%; Pred. No. 1.9e-191;  
 Matches 456; Conservative 81; Mismatches 91; Indels 17; Gaps 8;

QY 4 STATSPDGGTTFEHLWSSLEPDSYFDLPQSSRGNEVVGGT-----DSSMDVPH---L 54  
 DB 2 SQSSPADGGTTFEHLWSTLEPDSYFDLPQAGHSGRVSASSLPSNRAEVCMDVYMRDM 61  
 QY 55 EGMTTSVMAQNLSSSLSSMDQ--MSRAASAPYTPHAASVTPHSPVPSPTSFMSAP 113  
 DB 62 RMDNVNVSQSLSSNEQGLGNRAASTPSYSETTSNVTPTSPISQNSFTSAMSAP 121  
 QY 114 VPSNTDYPGPHFEVTFQSSSTAKSATWYSPLLKLYCQIAKTCPIQIKVSTPPPT 173  
 DB 122 AIPSTNDYPGPHFEVTFQSSSTAKSATWYSPLLKLYCQIAKTCPIQIKLASSPPNGS 181  
 QY 174 ATRAMPYTKAEHTVDVVKPCNHELGRDNFEGOSAPASHLRVEGNLSQYVDDPVTGR 233  
 DB 182 VIRAMPYTKAEHTVYVVKPCNHELGRDNFEGOSAPASHLRVEGNLSQYVDDPVTGR 241  
 QY 234 QSVWVYPPQVPGTFTILYNFNCSSCVGGMNRRLIITLEMRDGOVLGRSFGR 293  
 DB 242 QSAVLYEAPQVGTFTILYNFNCSSCVGGMNRRLIITLETRDGOVLGRSFGR 301  
 QY 294 ICACGRDRKADEHYREQOALNESSAKGAAKRAFKQSPAPALGAGVKKRRHGDE 353  
 DB 302 ICACGRDRKADEHYREQOALNESSAKGAAKRAFKQSPAPALGAGVKKRRHGDE 361  
 QY 354 TYLVQVRGRENFEILMKLESLELMELVLPQPLVDSYR--QQOQLQRPSPVPGVPLS 412  
 DB 362 MYIYVGRGRENFDILMKIDSLELVEYVQHFVDSYRQQOQLQRPSPVPGVPLS 421  
 QY 413 PMKVHGGMKNLPSVNLVQPPPHSSAATPNLGPVGMNNHGHAYPANGEMSSSSHA 472  
 DB 422 NNNKHGSIKSLPSVNLVQPPPHSSAATPNLGPVGMNNHGHAYPANGEMSSSSHA 479  
 QY 473 QSMVSGSHCTPPPHYHADPSLVFLGLGCPNCIEFTSQGLQSIYHLQNTIEDLGALK 532  
 DB 480 QSLVSTSHCTPPPHYHADPSLVFLGLGCPNCIEFTSQGLQSIYHLQNTIEDLGALK 539  
 QY 533 IPEQYRMTIWRGLQDLKQGHDSYTAQQLLR--SSNAATISIGSGELQORVMEVHFVR 591  
 DB 540 IPEQYRMTIWRGLQDLKQGHDSYTAQQLLR--SSNAATISIGSGELQORVMEVHFVR 597  
 QY 592 HTTIPNRGGPGGDEWADFGDLPCKARKQPIKEEFTAEIH 636  
 DB 598 HTTIPNRGGPGGDEWADFGDLPCKARKQPIKEEFTAEIH 641

## RESULT 5

Q9WUJ0 PRELIMINARY; PRT; 497 AA;  
 ID Q9WUJ0; AC Q9WUJ0; DT 01-NOV-1999 (TRENBLrel. 12, Created)  
 DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)  
 DT 01-OCT-2001 (TRENBLrel. 18, Last annotation update)  
 DE F73 (FRAGMENT); GN TRP73;  
 OS Mus musculus (Mouse); OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090; RN [1];  
 RP SEQUENCE FROM N.A.; RC STRAIN=D3 (129SV);  
 RX MEDLINE=99247549; PubMed=10232589;  
 RA Herranz M., Santos J., Salido E., Fernandez-Piqueras J., Serrano M.;  
 RT "Mouse p73 gene maps to the distal part of chromosome 4 and might be  
 RT involved in the progression of gamma-radiation-induced T-cell  
 RT lymphomas";  
 RL Cancer Res. 59:2068-2071(1999).  
 DR EMBL; AF138873; AAC32213.1; -;  
 DR HSSP; O15350; ICOK.  
 DR MGD; MGI:1336991; Trp73.  
 DR InterPro; IPR002117; P53.  
 DR InterPro; IPR001660; SAM.  
 DR Pfam; PF00870; P53; 1.  
 DR Pfam; PF00536; SAM; 1.  
 DR PRINTS; PR00386; P53SUPPRESSR.  
 DR Prodom; PD002681; P53; 1.  
 DR SMART; SM00454; SAM; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 497 AA; 54717 MW; 810C584F7D466025 CRC64;

Query Match 70.3%; Score 2379; DB 11; Length 497;  
 Best Local Similarity 90.2%; Pred. No. 1.2e-188;  
 Matches 450; Conservative 19; Mismatches 22; Indels 8; Gaps 5;  
 QY 144 YSPLLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPYKKAHVTDVVKRCPNHELGRDF 203  
 Db 1 YSPLLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPYKKAHVTDVVKRCPNHELGRDF 60  
 QY 204 NEGQAPASHLRVGNLSQVDDPVGTGROSVVVYEPVPGVGTFTILYNFMCNSSCV 263  
 Db 61 NEGQAPASHLRVGNLSQVDDPVGTGROSVVVYEPVPGVGTFTILYNFMCNSSCV 120  
 QY 264 GGNRRPILIIITLMDRGQVLGRSFEGRICACPGDRKADEHDYREQQALNESSAKNG 323  
 Db 121 GGNRRPILIIITLMDRGQVLGRSFEGRICACPGDRKADEHDYREQQALNESSAKNG 180  
 QY 324 ASKRAFKOSPAPVAPALGNGYKRRHGDDEYYIYQV-RGRENFEILMKLESLELMELVP 382  
 Db 181 ASKRAFKOSPAPVAPALGNGYKRRHGDDEYYIYQV-RGRENFEILMKLESLELMELVP 240  
 QY 383 QPLVDSYR--OQQLLRPSHLQPPSYGVLSPMNKHYGGNKLPSVNLVGGQPPHSSA 440  
 Db 241 QPLVDSYR--OQQLLRPSHLQPPSYGVLSPMNKHYGGNKLPSVNLVGGQPPHSSA 300  
 QY 441 ATPNLGVPGLNHNHGHAVPANGEMSSSSHAQSVSGSHCTPPPHADPPSLVSLTGL 500  
 Db 301 AGPNLPGMGSMLNHSNGHSPANGEMSGSSQTVSGSHCTPPPHADPPSLVSLTGL 360  
 QY 501 GCPNCEIYFTSGLOSIYHLQNLITLGLKALKEPQVYRWITWRGLQDLKQGHDYSTAQOL 560  
 Db 361 GCPNCEIYFTSGLOSIYHLQNLITLGLKALKEPQVYRWITWRGLQDLKQGHDYSTAQOL 418  
 QY 561 LR-SSNAATISGGSEGLQORQVMEAVHFRVHTITIPNRRGGPG--GPDENADFGDLP 617  
 Db 419 LRSSNAATISGGSEGLQORQVMEAVHFRVHTITIPNRRGGAGVTPGPDENADFGDLP 478

QY 618 DCKARKQPIKEEFTAEIHH 636  
 Db 479 DCKSRKQPIKEEFTETESH 497

## RESULT 6

Q9UP28 PRELIMINARY; PRT; 641 AA;  
 ID Q9UP28; AC Q9UP28; DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE TA P63 ALPHA; OS Homo sapiens (Human);  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606; RN [1];  
 RP SEQUENCE FROM N.A.; RX MEDLINE=98448095; PubMed=9774969;  
 RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,  
 RA Andrews N.C., Caput D., McKeon F.;  
 RT "p63, a p53 homolog at 3q27-29, encodes multiple products with  
 RT transactivating, death-inducing, and dominant-negative activities.";  
 RL Mol. Cell 2:305-316(1998).  
 DR EMBL; AF075430; AAC62635.1; -;  
 DR HSSP; P04637; IYCS.  
 DR InterPro; IPR002117; P53.  
 DR InterPro; IPR001660; SAM.  
 DR Pfam; PF00870; P53; 1.  
 DR PRINTS; PR00386; P53SUPPRESSR.  
 DR Prodom; PD002681; P53; 1.  
 DR SMART; SM00454; SAM; 1.  
 SQ SEQUENCE 641 AA; 72049 MW; 23A2E5EBAE63F605 CRC64;

Query Match 52.9%; Score 1790; DB 4; Length 641;  
 Best Local Similarity 55.1%; Pred. No. 1.1e-139;  
 Matches 366; Conservative 94; Mismatches 144; Indels 60; Gaps 18;  
 QY 1 MAQSTAT---SPDGGTTFEHLWSSLEP-----DSTVFDFLPQSSRGNNVVGTDSS 48  
 Db 1 MSQSTOTNEFLSPE---VFQIHWDFLEQICSVQPIDLNEVDFESEDGATNKT----EIS 53  
 QY 49 MDVFHLEGMTS-----VMAQFNLLSSTMDQSSRAASAPYTPHEAA-SVPHSPYAP 102  
 Db 54 MDCIRQDSDLDSPWPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAP 113  
 QY 103 SSTFDMSAPVIPSNTDYPGPHFEVTFQSSSTAKSATWTYSPLLKLYCQIAKTCPIQ 162  
 Db 114 SSTFDALSPAPISNTDYPGPHSFDVFSQSSSTAKSATWTYSELKLYCQIAKTCPIQ 173  
 QY 163 IKYSTPPPGTAIRAMPYKKAHVTDVVKRCPNHELGRDFNEGQAPASHLRVGNLS 222  
 Db 174 IKVTPPGAVIRAMPYKKAHVTEVVKRCPNHELGRDFNEGQAPASHLRVGNLS 233  
 QY 223 SQYVDPVGTGROSVVVYEPVPGVGTFTILYNFMCNSSCVGGNRRPILIIITLMDRG 282  
 Db 234 AQVDEPIITGROSLVLPVYEPVPGVGTFTILYNFMCNSSCVGGNRRPILIIITLMDRG 293  
 QY 283 QVLGRSFEGRICACPGDRKADEHDYREQQALNESSAKNGASKRAFKOSPAPVAPALGA 342  
 Db 294 QVLGRSFEGRICACPGDRKADEHDYREQQALNESSAKNGASKRAFKOSPAPVAPALGA 349  
 QY 343 GVKRRHGDDEYYIYQV-RGRENFEILMKLESLELMELVPPLVDSYRQOQ-----LLQ 397  
 Db 350 SIKKRSPPDELLYLPVRGRETYEMLLIKESLELMOYLPOHTIETYRQOQOQHLLQ 409  
 QY 398 RPSHLQ-PPSYGVLSPMNKHYGGNKLPSVNLVGGQPPHSSAATPNLGPVPGP-----M 452  
 Db 410 KQTSISPSGSPNPLNKN-SMNKLPYSQLIN--PQORNALPTTTPDGMGANIPM 466  
 QY 453 LNNHGHAVPANGEMSS5HSAQ-----SMVSGSHCTPPPHADPPSLVSLTGLGCPNCI 506

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Db 467 MGTH---MPMAGDMNGLSPTQALPPPLSMPSTSHCTPPPTDCSIVSFLARLGSSCL 523
QY 507 EYFTSGLOSIYHLQNLIEDLGALKIPEQYRMTIWRGLQDLKQGHYDSTAQOLLRS-SN 565
Db 524 DYFTQGLTIIQIYEHYSMDLAKIPEQFRHAIWKIILDHQKLEHFFSPLLTPSS 583
QY 566 AATISIGSGELQORVMEAVHFRVHTITIPNRGGPGGPGDWADEFGDLDPCKARKQP 625
Db 584 ASTVSV-GSSETRGERVIDAVRFTLQTIISPPR-----DEWDFNFDMDARRNKQOR 635
QY 626 IKKE 629
Db 636 IKKE 639

RESULT 7
Q9H3D4 ID Q9H3D4 PRELIMINARY; PRT; 680 AA.
AC Q9H3D4;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE TA P63 ALPHA.
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKee F.,
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities."
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hagiwara K., McKenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF124539; AAG45607.1; JOINED.
DR EMBL; AF124528; AAG45607.1; JOINED.
DR EMBL; AF124529; AAG45607.1; JOINED.
DR EMBL; AF124531; AAG45607.1; JOINED.
DR EMBL; AF124532; AAG45607.1; JOINED.
DR EMBL; AF124533; AAG45607.1; JOINED.
DR EMBL; AF124534; AAG45607.1; JOINED.
DR EMBL; AF124535; AAG45607.1; JOINED.
DR EMBL; AF124536; AAG45607.1; JOINED.
DR EMBL; AF124537; AAG45607.1; JOINED.
DR EMBL; AF124538; AAG45607.1; JOINED.
DR HSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001560; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; UNKNOWN.1.
SQ SEQUENCE 680 AA; 76785 MW; F66EBCD45E87D9799 CRC64;

Query Match 52.9%; Score 1790; DB 4; Length 680;
Best Local Similarity 55.1%; Pred. No. 1.2e-139;
Matches 366; Conservative 94; Mismatches 144; Indels 60; Gaps 18;

QY 1 MAQSTAT-----SPDGGTTFEHLWSSLEP-----DSYFDLPQSSRGNEVGGTDS 48
Db 40 MSQQTQNEFLSPE---VFQIHDFLEQPCISVQPIDLNFVDEPSEDGATNKI----EIS 92
QY 49 MDVTHFGMTS-----VMAQFNLLSTMDQMSRAASAPYTPPEHAA-SVPTHSPTAQP 102
Db 93 MDCIRMODSLSDPMPWQYTNLGLNMDQIQNGSSSTSPNTDHAQNSVTPSPYAQP 152

QY 103 STFTDMSAPVPIPSNTDYPGPHFHEVTFQOSSTAKSATWTYSPLLKLYCQIAKTCPIQ 162
Db 153 STFDALSPSPAIPSTNDYPGPHSFDVSFQOSSTAKSATWTYSTELKLYCQIAKTCPIQ 212
QY 163 IKYSTPPPGTAIRAMPYKKAHVTDVVKPCNHELGRDFNFGOSAPASHLLRVRGNL 222
Db 213 IKYMTPPPGAVIRAMPYKKAHVTEVVKPCNHELGRDFNFGOSAPASHLLRVRGNL 272
QY 223 SOYVDDPVGROSVVVPEPQGVTEFTTILYFNCMSSCVGGNNRRPILIIITLEMRDG 282
Db 273 AQVVEDPIGRQSLVLPVPEPQGVTEFTTILYFNCMSSCVGGNNRRPILIIITLETRDG 332
QY 283 QVLGRSFEGRICACPGDRKADDEHYEQQALNESSAKNGAKSKAFKQSPVAPALGA 342
Db 333 QVLGRRCFEARICACPGDRKADDEHSIRKQV--SDSTKNGDGTFRFRFNTHTGIGM--T 388
QY 343 GVKRRHGDDETYILQVRGRENFEILMKLESLELMELVPOPLVDSYRQOQ-----LIQ 397
Db 389 SIKKRSPPDELLYLPVGRRETYEMLLAIKESLELMQYLPQHTTETVROQQOQHQLLQ 448
QY 398 RPSHLQ-PPSYGVLSPMKNVHGKMLPSVNLVQGPVPPHSSAATENLGPVGP-----M 452
Db 449 KQTSIQSPSSYGNSSPPLNKN--SMNKLPSVSQLIN--POQRNALTTTIPDGMGANIPM 505
QY 453 LNNHGHAVPANGEMSSSSHAQ-----SMVSGSHCTPPPYHADPSVLSVLTGLGCPNCI 506
Db 506 MGTH---MPMAGDMNGLSPTQALPPPLSMPSTSHCTPPPTDCSIVSFLARLGSSCL 562
QY 507 EYFTSGLOSIYHLQNLIEDLGALKIPEQYRMTIWRGLQDLKQGHYDSTAQOLLRS-SN 565
Db 563 DYFTQGLTIIQIYEHYSMDLAKIPEQFRHAIWKIILDHQKLEHFFSPLLTPSS 622
QY 566 AATISIGSGELQORVMEAVHFRVHTITIPNRGGPGGPGDWADEFGDLDPCKARKQP 625
Db 623 ASTVSV-GSSETRGERVIDAVRFTLQTIISPPR-----DEWDFNFDMDARRNKQOR 674
QY 626 IKKE 629
Db 675 IKKE 678

RESULT 8
Q99JE3 ID Q99JE3 PRELIMINARY; PRT; 663 AA.
AC Q99JE3;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE TA1 KET ALPHA PROTEIN.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=TONGUE.
RX MEDLINE=21363378; PubMed=11470269;
RA Bamberger C., Schmale H.;
RT "Identification and tissue distribution of novel KET/p63 splice
RT variants."
RL FEBS Lett. 501:121-126(2001).
DR EMBL; AJ277446; CAC37098.1; -.
DR HSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; UNKNOWN.1.
SQ SEQUENCE 663 AA; 74660 MW; C953BBAC389D5B70 CRC64;

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Query Match 52.9%; Score 1789; DB 11; Length 663;  
Best Local Similarity 55.1%; Pred. No. 1.4e-139;  
Matches 366; Conservative 93; Mismatches 145; Indels 60; Gaps 18;

QY 1 MAQSTAT-----SPDGGTTFEHLWSLEP-----DSTVFDLPQSSRGNNEVVGTDSS 48  
DB 23 MSOSTOTSEFLSPE---VFQIHWDFLEQPCISVQPIELNFVDEPSENGATNKI-----EIS 75

QY 49 MDVFLHGTTS-----VMAQFNLLSMDQMSRAASAPYTPPEHAA-SVTPHSPYAPQ 102  
DB 76 MDCIRMQSDLSDPMPQYTNLGLNMDQIQNGSSSTSPYNTDHAQNSVTPAPSYAPQ 135

QY 103 STFTDMSPPAPVIPNTDYPGPHFEVTFQSSSTAKSATWTYSPLKLYCQIAKTCPIQ 162  
DB 136 SSTDALSPPAIPNTDYPGPHFEVTFQSSSTAKSATWTYSPLKLYCQIAKTCPIQ 195

QY 163 IKVSTPPPGTAIRAMPYVYKAEHVTVKRCNHELGRDNFEGQAPASHLIRVEGNL 222  
DB 196 IKVSTPPPGTAIRAMPYVYKAEHVTVKRCNHELGRDNFEGQAPASHLIRVEGNL 255

QY 223-SQVDDPVTGROSVVVPYEPQVGTFTTILYNPNCSSCVGGMNRRPILITILEMRDG 282  
DB 256 AQVEDPITGROSVLVPEPQVGTFTTILYNPNCSSCVGGMNRRPILITILEMRDG 315

QY 283 QVLRGRSFEGRICACPGDRKADDEHYREQALNESAASAKRAKFPAPVAPALGA 342  
DB 316 QVLRGRSFEGRICACPGDRKADDEHYREQALNESAASAKRAKFPAPVAPALGA 371

QY 343 GVKRRHGDEYVYLVQVGRNFEFLMKLESLELMELVQPLVDVSYRQOOQ-----LIQ 397  
DB 372 SIKRRSPDDELLYPVGRRETYEMLLKESLELMELVQPLVDVSYRQOOQOOHQLQ 431

QY 398 RPSHLQ-PPSYGPIVSPMKNVHGKMLPSVNLVGGPPPHSSAATPNLGPVGP-----M 452  
DB 432 KOTSMOSQSSYGNSSPPLNKN-SMNLKPSVSLIN--POORNALPTTMEGMGANIPM 488

QY 453 LNNHGHAVPANGEMSSSSHAQ-----SMVSGSHCTPPPPYHADPSLVFLTGLGCPNCI 506  
DB 489 MGTHT---MPMAGDMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCL 545

QY 507 EYFTSOGLOSIVHLQNLITIEDLGALKIPEQYRMTIWRGLQDQKGDYSTAQQLRS-SN 565  
DB 546 DYFTTQGLTIIQIHYSMDDLASLKIPEQYRMTIWRGLQDQKGDYSTAQQLRS-SN 605

QY 566 AATISIGSGELQORVMEVHFRVHTITIPNRRGGGGGDEWADFGDLPCKARKOP 625  
DB 606 ASIVSV-GSSETRGERVIDAVRFLRTQISFPFR-----DEWDFNDFMDSRRNKQOR 657

QY 626 IKEE 629  
DB 658 IKEE 661

RESULT 9  
O8898 ID O8898 PRELIMINARY; PRT; 680 AA.  
AC O8898;  
DT 01-NOV-1998 (TRENBLrel. 08, Created)  
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE TA\*P63 ALPHA.  
GN TRP63.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
ON NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98448095; PubMed=9774969;  
RA Yang A., Raghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,  
RA Caput D., McKoon F.;  
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with  
transactivating, death-inducing, and dominant-negative activities."

RL Mol. Cell 2:305-316(1998).  
DR EMBL; AF075436; AAC62641.1; -  
DR HSSP; P04637; 1YCS.  
DR MGD; MGI:1330810; Trp63.  
DR InterPro; IPR002117; P53.  
DR InterPro; IPR001660; SAM.  
DR Pfam; PF00870; P53; 1.  
DR PRINTS; PR00386; P53SUPPRESSR.  
DR ProDom; PD002681; P53; 1.  
DR SMART; SM00454; SAM; 1.  
SQ SEQUENCE 680 AA; 76788 MW; 8DF0284F247C68A CRC64;

Query Match 52.9%; Score 1789; DB 11; Length 680;  
Best Local Similarity 55.1%; Pred. No. 1.4e-139;  
Matches 366; Conservative 94; Mismatches 144; Indels 60; Gaps 18;

QY 1 MAQSTAT-----SPDGGTTFEHLWSLEP-----DSTVFDLPQSSRGNNEVVGTDSS 48  
DB 40 MSOSTOTSEFLSPE---VFQIHWDFLEQPCISVQPIELNFVDEPSENGATNKI-----EIS 92

QY 49 MDVFLHGTTS-----VMAQFNLLSMDQMSRAASAPYTPPEHAA-SVTPHSPYAPQ 102  
DB 93 MDCIRMQSDLSDPMPQYTNLGLNMDQIQNGSSSTSPYNTDHAQNSVTPAPSYAPQ 152

QY 103 STFTDMSPPAPVIPNTDYPGPHFEVTFQSSSTAKSATWTYSPLKLYCQIAKTCPIQ 162  
DB 153 SSTDALSPPAIPNTDYPGPHFEVTFQSSSTAKSATWTYSPLKLYCQIAKTCPIQ 212

QY 163 IKVSTPPPGTAIRAMPYVYKAEHVTVKRCNHELGRDNFEGQAPASHLIRVEGNL 222  
DB 213 IKVSTPPPGTAIRAMPYVYKAEHVTVKRCNHELGRDNFEGQAPASHLIRVEGNL 272

QY 223-SQVDDPVTGROSVVVPYEPQVGTFTTILYNPNCSSCVGGMNRRPILITILEMRDG 282  
DB 273 AQVEDPITGROSVLVPEPQVGTFTTILYNPNCSSCVGGMNRRPILITILEMRDG 332

QY 283 QVLRGRSFEGRICACPGDRKADDEHYREQALNESAASAKRAKFPAPVAPALGA 342  
DB 333 QVLRGRSFEGRICACPGDRKADDEHYREQALNESAASAKRAKFPAPVAPALGA 388

QY 343 GVKRRHGDEYVYLVQVGRNFEFLMKLESLELMELVQPLVDVSYRQOOQ-----LIQ 397  
DB 389 SIKRRSPDDELLYPVGRRETYEMLLKESLELMELVQPLVDVSYRQOOQOOHQLQ 448

QY 398 RPSHLQ-PPSYGPIVSPMKNVHGKMLPSVNLVGGPPPHSSAATPNLGPVGP-----M 452  
DB 449 KOTSMOSQSSYGNSSPPLNKN-SMNLKPSVSLIN--POORNALPTTMEGMGANIPM 505

QY 453 LNNHGHAVPANGEMSSSSHAQ-----SMVSGSHCTPPPPYHADPSLVFLTGLGCPNCI 506  
DB 506 MGTHT---MPMAGDMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCL 562

QY 507 EYFTSOGLOSIVHLQNLITIEDLGALKIPEQYRMTIWRGLQDQKGDYSTAQQLRS-SN 565  
DB 563 DYFTTQGLTIIQIHYSMDDLASLKIPEQYRMTIWRGLQDQKGDYSTAQQLRS-SN 622

QY 566 AATISIGSGELQORVMEVHFRVHTITIPNRRGGGGGDEWADFGDLPCKARKOP 625  
DB 623 ASIVSV-GSSETRGERVIDAVRFLRTQISFPFR-----DEWDFNDFMDSRRNKQOR 674

QY 626 IKEE 629  
DB 675 IKEE 678

RESULT 10  
O9JJP6 ID O9JJP6 PRELIMINARY; PRT; 680 AA.  
AC O9JJP6;  
DT 01-OCT-2000 (TRENBLrel. 15, Created)  
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE TA2 KET ALPHA.





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Db 114 SSTFDALSPSPALPSNTDYPGPHSFDFVFSQOSTAKSATWYSTELKKLYCOIAKTCPIQ 173
QY 163 IKVSTPPPGPAIRAMPVYKAEHVTDVRCNHELGRDFNEGOSAPASHLIRVEGNL 222
Db 174 IKVSTPPPGPAIRAMPVYKAEHVTDVRCNHELGRDFNEGOSAPASHLIRVEGNL 233
QY 223 SOYVDDPVTGRQSVVVPYEPQVGTETTYLYNFMCSNCSVGMNRRPILIIITLEM RDG 282
Db 234 AQYVEDPITGRQSVLVPEYEPQVGTETTYLYNFMCSNCSVGMNRRPILIIITLEM RDG 293
QY 293 QVLRGRSEGRICACPGDRKADDEHYREOQALNESAANKRAKFPQSPVAPALGA 342
Db 294 QVLRGRSEGRICACPGDRKADDEHYREOQALNESAANKRAKFPQSPVAPALGA 349
QY 343 GYKRRHDEDTYLYOVRGRENFEILMKLESLMELVPOPLVDYSYRQOQO-----LLQ 397
Db 350 SIKKRSPPDELLLYLVGRRETYEMLLKIKESLELMQYLPOHTIETRYQOQOQHLLQ 409
QY 398 RPSHLQ-PPSYGVLSPMKNVHGMMKLPVNLVQPPPHSSAATPNLGPVGP-----M 452
Db 410 KQTSIQSPSSYGNSSPPLNKMN-SMNKLPVSQLIN--PQORNALTPPTIPDGMGANIPM 466
QY 453 LNNHGHAVPANGEMSSSHSAQ-----SMVSGSHCTPPPPYHADPSLVSFLTGLGCPNCI 506
Db 467 MGTH---NPMAGDMNGLSPQALPPPLSMFSTSHCTPPPPYPTDCSIVGLARLGCSSCL 523
QY 507 EYFTSQGLQSIYHLQNTIEDLGALKIPEQRYMTIWRGLQDLKQGHDYSTAQQLRS-SN 565
Db 524 DYFTQGLTTIYQEHYSMDLASLKIPEQRYMTIWRGLQDLKQGHDYSTAQQLRS-SN 583
QY 566 AATISIGSGELQRYVMEVHFVRHTITIPNRGPGGPGDEWADFDLPDCKARKQP 625
Db 584 ASTVSV-GSSETRGVIDAVRFLRTQISFPFR-----DEWDFNDFMDARANKQOR 635
QY 626 IKEE 629
Db 636 IKEE 639

RESULT 12
Q9UE10 PRELIMINARY; PRT; 680 AA.
AC Q9UE10;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE KET PROTEIN.
GN KET.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SKELETAL MUSCLE AND KERATINOCYTE CULTURE;
RX MEDLINE-99018225; PubMed-9799841;
RA Augustin M., Bamberger C., Paul D., Schmale H.;
RT "Cloning and chromosomal mapping of the human p53-related KET gene to
RL Mamm. Genome 9:899-902(1998).
DR EMBL; Y16961; CAA76562.1;
DR HSSP; P04637; IYCS
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PD00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
SQ SEQUENCE 680 AA; 76776 MW; 6548A6F2187D852E CRC64;

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Query Match 52.7%; Score 1782; DB 4; Length 680;  
 Best Local Similarity 55.0%; Pred. No. 5.3e-139;  
 Matches 365; Conservative 94; Mismatches 145; Indels 60; Gaps 18;

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QY 1 MAQSTAT-----SPDGGTTFEHLMSLEP-----DSTYFDLPSSRGNNNEVVGTDSS 48
Db 40 MSQSTQTFNEFLSPE---VFQIHWDFLEQPCSVQPIDLNFDVDEPSEDGATNKI-----EIS 92
QY 49 MDVFHLEGMTTS-----VMAQFNLLSTMDQSSRAASASPYTPPEHAA-SVPTHTSPYAPQ 102
Db 93 MDCIRKQSDLSDPMPQYTNLGLNMQOIQNGSSSIPYNTDHAQNSVTAPSPYAPQ 152
QY 103 SSTFTMSPAVPIPSNTDYPGPHHFEVTFQOSTAKSATWYSTELKKLYCOIAKTCPIQ 162
Db 153 SSTFDALSPSPALPSNTDYPGPHSFDFVFSQOSTAKSATWYSTELKKLYCOIAKTCPIQ 212
QY 163 IKVSTPPPGPAIRAMPVYKAEHVTDVRCNHELGRDFNEGOSAPASHLIRVEGNL 222
Db 213 IKVSTPPPGPAIRAMPVYKAEHVTDVRCNHELGRDFNEGOSAPASHLIRVEGNL 272
QY 223 SOYVDDPVTGRQSVVVPYEPQVGTETTYLYNFMCSNCSVGMNRRPILIIITLEM RDG 282
Db 273 AQYVEDPITGRQSVLVPEYEPQVGTETTYLYNFMCSNCSVGMNRRPILIIITLEM RDG 332
QY 283 QVLRGRSEGRICACPGDRKADDEHYREOQALNESAANKRAKFPQSPVAPALGA 342
Db 333 QVLRGRSEGRICACPGDRKADDEHYREOQALNESAANKRAKFPQSPVAPALGA 388
QY 343 GYKRRHDEDTYLYOVRGRENFEILMKLESLMELVPOPLVDYSYRQOQO-----LLQ 397
Db 389 SIKKRSPPDELLLYLVGRRETYEMLLKIKESLELMQYLPOHTIETRYQOQOQHLLQ 448
QY 398 RPSHLQ-PPSYGVLSPMKNVHGMMKLPVNLVQPPPHSSAATPNLGPVGP-----M 452
Db 449 KQTSIQSPSSYGNSSPPLNKMN-SMNKLPVSQLIN--PQORNALTPPTIPDGMGANIPM 505
QY 453 LNNHGHAVPANGEMSSSHSAQ-----SMVSGSHCTPPPPYHADPSLVSFLTGLGCPNCI 506
Db 506 MGTH---NPMAGDMNGLSPQALPPPLSMFSTSHCTPPPPYPTDCSIVGLARLGCSSCL 562
QY 507 EYFTSQGLQSIYHLQNTIEDLGALKIPEQRYMTIWRGLQDLKQGHDYSTAQQLRS-SN 565
Db 563 DYFTQGLTTIYQEHYSMDLASLKIPEQRYMTIWRGLQDLKQGHDYSTAQQLRS-SN 622
QY 566 AATISIGSGELQRYVMEVHFVRHTITIPNRGPGGPGDEWADFDLPDCKARKQP 625
Db 623 ASTVSV-GSSETRGVIDAVRFLRTQISFPFR-----DEWDFNDFMDARANKQOR 674
QY 626 IKEE 629
Db 675 IKEE 678

RESULT 13
O89097 PRELIMINARY; PRT; 586 AA.
AC O89097;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE DN P63 ALPHA.
GN TRP63 OR P73H.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98448095; PubMed-9774969;
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities."
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.

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|                       |        |  |           |            |      |        |      |
|-----------------------|--------|--|-----------|------------|------|--------|------|
| Query Match           | 51.4%  | Score  | 1740;     | DB         | 11;  | Length | 586; |
| Best Local Similarity | 58.1%; | Pred. No.  | 1.3e-135; |            |      |        |      |
| Matches               | 348;   | Conservative   | 86;       | Mismatches | 121; | Indels | 44;  |
|                       |        |  |           | Gaps       |      |        | 14;  |
| QY                    | 57     | MTSYMAQFN-----LLSSTWDQSSRAASAPYTPHAA-SYPTTHSPYQAQSSFTD       | 107       |            |      |        |      |
| Db                    | 4      | LESNAQTQFSEFQVYTNGLLNGMDQIQNGSSSTSYNTDHAQNSVYAPSPYAQSSFTD    | 63        |            |      |        |      |
| QY                    | 108    | TWSPAPVTPSNTDYPGPHFEVTFQQSSTAKSATWYSPLLKLYCQIAKTCPIQIKYST    | 167       |            |      |        |      |
| Db                    | 64     | ALSPSPAIPSTNDYPGPHSFDFVQQSSTAKSATWYSTELKKLYCQIAKTCPIQIKWMT   | 123       |            |      |        |      |
| QY                    | 168    | PPPTGTAIRAMPVYKKAEBHTDVVKRCPNHELGRDFNEGOSAPASHLIRVEGNLSQYVD  | 227       |            |      |        |      |
| Db                    | 124    | PPQOGAVIRAMPVYKKAEBHTEVVKRCPNHELGRDFNEGQIAPPSHLIRVEGNSHAQYVE | 183       |            |      |        |      |
| QY                    | 228    | DPVTCROSVVYPPEPPQVGTFTTILYFNWCNSSCVGGNNRRPILIIILEMRDQGVLR    | 287       |            |      |        |      |
| Db                    | 184    | DPITGRQSVLYPPEPPQVGTFTTILYFNWCNSSCVGGNNRRPILIVTLETNRDQGVLR   | 243       |            |      |        |      |
| QY                    | 288    | RSFEGRICACPRKAKADEHYRQQALESNAKGAASAKRAFPQSPAPVAPGALGVYKR     | 347       |            |      |        |      |
| Db                    | 244    | RCFEARICACPRKAKADESIRKQOV--SDSAKNGDGTKRPRFQTHGIQM--TSIKKR    | 299       |            |      |        |      |
| QY                    | 348    | RHGDEDTYYLVQRGRENFEILMKLKELEMLYPLVDYSYRQOQ-----LLQRPSHL      | 402       |            |      |        |      |